

Janjira Phavaphutanon 2009: Quantitative Trait Loci Mapping for Canine Hip Dysplasia. Doctor of Philosophy (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program.
Thesis Advisor: Associate Professor Theerapol Sirinarumitr, Ph.D. 160 pages.

Canine hip dysplasia is a common complex disease, the secondary effects of which cause debilitating hip osteoarthritis. To locate the quantitative trait loci (QTL) that contribute to canine hip dysplasia, 159 crossbred and 192 purebred Labrador Retrievers were analyzed. Hip trait was measured using 4 radiographic methods: the Norberg angle, the dorsolateral subluxation score, the distraction index and OFA score. A genome-wide screening was undertaken at 428 and 284 unique microsatellite loci in crossbred and purebred Labrador Retrievers, respectively. The results from the genome-wide screening identified 11 regions i.e. CFA02, 03, 04, 05, 06, 09, 10, 11, 16, 29 and 37 in crossbred and 6 regions i.e. CFA01, 02, 10, 20, 22 and 32 in purebred Labrador Retrievers that harbored significant ($p < 0.05$) putative QTLs associating with hip dysplasia at LOD scores > 2.0 . Two chromosomal regions (CFA11 and 29) from the genome-wide screening were chosen for fine mapping with SNP markers to narrow down the QTL position. The analysis result revealed QTL at 19.7 cM and 19.6 cM for DIL and DIR on CFA11 and at 20.3 cM for DIL and 2 QTL for DIR at 20.3 and at 21 cM in CFA29, respectively. The aim of QTL mapping is to apply genetic testing and marker-assisted selection that may improve susceptibility of hip trait screening at a very young age. Genetic testing should assist in preventing carriers with mutant alleles from entering the genetic pool before breeding time and thus decrease the incidence of the disease.

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Thesis Advisor's signature

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